

## SEQUENCE LISTING

<110> RIKEN  
KABUSHIKI KAISHA DNAFORM

<120> Method for utilizing the 5' end of mRNA for cloning and analysis

<130> 1336(PCT)

<150> JP 2002-171851  
<151> 2002-06-12

<150> JP 2002-235294  
<151> 2002-08-12

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<170> PatentIn version 3.1

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 aaccgcaccg tcggacctag gtccgacgga aaagcagctt cctccactct aggtccgacg 300  
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Leu Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys			210			215					220					
tcc tgt gac agc agg gat aac aca ctg caa gtg gac atc aac ggg ttc	1561															
Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe			225			230			235				240			
act acc ggc cgc cga ggt gac ctg gcc acc att cat ggc atg aac cgg	1609															
Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg			245					250					255			
cct ttc ctg ctt ctc atg gcc acc ccg ctg gag agg gcc cag cat ctg	1657															
Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu			260					265					270			
caa agc tcc cgg cac cgc cga gcc ctg gac acc aac tat tgc ttc agc	1705															
Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser			275					280					285			

tcc acg gag aag aac tgc tgc gtg cgg cag ctg tac att gac ttc cgc 1753  
 Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg  
 290 295 300

aag gac ctc ggc tgg aag tgg atc cac gag ccc aag ggc tac cat gcc 1801  
 Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala  
 305 310 315 320

aac ttc tgc ctc ggg ccc tgc ccc tac att tgg agc ctg gac acg cag 1849  
 Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln  
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tac agc aag gtc ctg gcc ctg tac aac cag cat aac cgg ggc gcc tcg 1897  
 Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser  
 340 345 350

gcg gcg ccg tgc tgc gtg ccg cag gcg ctg gag ccg ctg ccc atc gtg 1945  
 Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val  
 355 360 365

tac tac gtg ggc cgc aag ccc aag gtg gag cag ctg tcc aac atg atc 1993  
 Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile  
 370 375 380

gtg cgc tcc tgc aag tgc agc tga ggtccccccc cgccccggcc cgccccggca 2047  
 Val Arg Ser Cys Lys Cys Ser  
 385 390

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 <212> PRT  
 <213> Homo sapiens

<400> 77

Met Pro Pro Ser Gly Leu Arg Leu Leu Pro Leu Leu Leu Pro Leu Leu  
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Trp Leu Leu Val Leu Thr Pro Gly Pro Pro Ala Ala Gly Leu Ser Thr  
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Cys Lys Thr Ile Asp Met Glu Leu Val Lys Arg Lys Arg Ile Glu Ala

35

40

45

Ile Arg Gly Gln Ile Leu Ser Lys Leu Arg Leu Ala Ser Pro Pro Ser  
50 55 60

Gln Gly Glu Val Pro Pro Gly Pro Leu Pro Glu Ala Val Leu Ala Leu  
65 70 75 80

Tyr Asn Ser Thr Arg Asp Arg Val Ala Gly Glu Ser Ala Glu Pro Glu  
85 90 95

Pro Glu Pro Glu Ala Asp Tyr Tyr Ala Lys Glu Val Thr Arg Val Leu  
100 105 110

Met Val Glu Thr His Asn Glu Ile Tyr Asp Lys Phe Lys Gln Ser Thr  
115 120 125

His Ser Ile Tyr Met Phe Phe Asn Thr Ser Glu Leu Arg Glu Ala Val  
130 135 140

Pro Glu Pro Val Leu Leu Ser Arg Ala Glu Leu Arg Leu Leu Arg Arg  
145 150 155 160

Leu Lys Leu Lys Val Glu Gln His Val Glu Leu Tyr Gln Lys Tyr Ser  
165 170 175

Asn Asn Ser Trp Arg Tyr Leu Ser Asn Arg Leu Leu Ala Pro Ser Asp  
180 185 190

Ser Pro Glu Trp Leu Ser Phe Asp Val Thr Gly Val Val Arg Gln Trp  
195 200 205

Leu Ser Arg Gly Gly Glu Ile Glu Gly Phe Arg Leu Ser Ala His Cys  
210 215 220

Ser Cys Asp Ser Arg Asp Asn Thr Leu Gln Val Asp Ile Asn Gly Phe  
225 230 235 240

Thr Thr Gly Arg Arg Gly Asp Leu Ala Thr Ile His Gly Met Asn Arg  
245 250 255

Pro Phe Leu Leu Leu Met Ala Thr Pro Leu Glu Arg Ala Gln His Leu  
260 265 270

Gln Ser Ser Arg His Arg Arg Ala Leu Asp Thr Asn Tyr Cys Phe Ser  
275 280 285

Ser Thr Glu Lys Asn Cys Cys Val Arg Gln Leu Tyr Ile Asp Phe Arg  
290 295 300

Lys Asp Leu Gly Trp Lys Trp Ile His Glu Pro Lys Gly Tyr His Ala  
305 310 315 320

Asn Phe Cys Leu Gly Pro Cys Pro Tyr Ile Trp Ser Leu Asp Thr Gln  
325 330 335

Tyr Ser Lys Val Leu Ala Leu Tyr Asn Gln His Asn Pro Gly Ala Ser  
340 345 350

Ala Ala Pro Cys Cys Val Pro Gln Ala Leu Glu Pro Leu Pro Ile Val  
355 360 365

Tyr Tyr Val Gly Arg Lys Pro Lys Val Glu Gln Leu Ser Asn Met Ile  
370 375 380

Val Arg Ser Cys Lys Cys Ser  
385 390